09/578,693
LVCook 12/27/04

(FILE 'HOME' ENTERED AT 20:50:54 ON 24 DEC 2004)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, CANCERLIT, JAPIO' ENTERED AT 20:51:16 ON 24 DEC 2004

L1	6331	S	FABP?
L2	2140	S	L1 AND LIVER?
L3	927	S	(L FABP)
L4	20	S	L3 AND RENAL?
L5	38	S	L3 AND KIDNEY?
L6	12	DUPLICATE REMOVE	L4 (8 DUPLICATES REMOVED)
L7	25	DUPLICATE REMOVE	L5 (13 DUPLICATES REMOVED)

=>

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FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, CANCERLIT, JAPIO' ENTERED AT 20:51:16 ON 24 DEC 2004

L1 6331 S FABP?
L2 2140 S L1 AND LIVER?
L3 927 S (L FABP)
L4 20 S L3 AND RENAL?
L5 38 S L3 AND KIDNEY?
L6 12 DUPLICATE REMOVE L4 (8 DUPLICATES REMOVED)
L7 25 DUPLICATE REMOVE L5 (13 DUPLICATES REMOVED)

=>

ANSWER 20 OF 25 MEDLINE on STN
AN 93352664 MEDLINE
DN PubMed ID: 8349710
TI Use of transgenic mice to map cis-acting elements in the liver fatty acid-binding protein gene (Fabpl) that regulate its cell lineage-specific, differentiation-dependent, and spatial patterns of expression in the gut epithelium and in the liver acinus.
AU Simon T C; Roth K A; Gordon J I
CS Department of Molecular Biology, Washington University School of Medicine, St. Louis, Missouri 63110.
NC DK30292 (NIDDK)
SO Journal of biological chemistry, (1993 Aug 25) 268 (24) 18345-58.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199309
ED Entered STN: 19931001
Last Updated on STN: 19931001
Entered Medline: 19930916
AB Axial pattern formation is sustained in the mammalian gut epithelium despite rapid and continuous renewal of its four principal cell lineages. The mouse and rat liver fatty acid-binding protein (**L-FABP**) genes (Fabpl) represent an excellent model for understanding the mechanisms that determine differentiation-dependent, cell lineage-specific, and distinct regional patterns of expression along the crypt-to-villus and duodenal-to-ileal axes of the gut, as well as within the liver acinus. We have used transgenic mice to map cis-acting elements in rat Fabpl that control these patterns of gene expression. Seven transgenes were analyzed, representing sequential deletions of the 5'-nontranscribed domain of Fabpl linked to the human growth hormone (hGH) gene beginning at its nucleotide +3 (**L-FABP**/hGH+3). Several pedigrees of mice containing each one of the **L-FABP**/hGH+3 transgenes were examined at the end of their 8th and 20th weeks of postnatal life using immunocytochemical and RNA hybridization analyses. A remarkably compact sequence spanning nucleotides -132 to +21 of Fabpl is sufficient to establish and maintain a distribution of reporter mRNA and protein in villus-associated enterocytes located along the duodenal-to-ileal axis of the gut that resembles the pattern of expression of the endogenous Fabpl gene. **L-FABP**-132 to +21/hGH+3 is also expressed in surface and pit mucous cells of gastric units and in enterocytes located in the colonic homologs of small intestinal villi, the surface epithelial cuffs. This pattern of transgene expression in the stomach and colon recapitulates that of the intact endogenous donor rat Fabpl but not that of mouse Fabpl, which is silent in these proximal and distal segments of the gastrointestinal tract. Analysis of mice containing **L-FABP**-4000 to +21/hGH+3, **L-FABP**-1600 to +21/hGH+3, **L-FABP**-596 to +21/hGH+3, **L-FABP**-246 to +21/hGH+3, and **L-FABP**-186 to +21/hGH+3 indicate that Fabpl's cephalocaudal gradient is influenced by cis-acting suppressors of cecal and colonic expression located between nucleotides -4000 and -1600 and by cis-acting activators of cecal and colonic expression located between nucleotides -597 and -351. **L-FABP**-132 to +21/hGH+3 is precociously activated in proliferating and nonproliferating epithelial cells located in intestinal crypts. The suppressor(s) of **L-FABP** accumulation in crypt epithelial cell populations are not represented between nucleotides -4000 and +21, indicating that different cis-acting sequences regulate regional and differentiation-dependent patterns of Fabpl expression.(ABSTRACT TRUNCATED AT 400 WORDS)
CT Aging: ME, metabolism

Animals
Base Sequence
*Carrier Proteins: BI, biosynthesis
*Carrier Proteins: GE, genetics
Cell Differentiation
Digestive System: CY, cytology
*Digestive System: ME, metabolism
Epithelial Cells
Epithelium: ME, metabolism
Fatty Acids: ME, metabolism
Growth Hormone: BI, biosynthesis
Growth Hormone: BL, blood
Growth Hormone: GE, genetics
Humans
Immunohistochemistry
In Situ Hybridization
Kidney: CY, cytology
Kidney: ME, metabolism
Liver: CY, cytology
*Liver: ME, metabolism
Mice
Mice, Transgenic
Molecular Sequence Data
*Neoplasm Proteins
*Nerve Tissue Proteins
Oligodeoxyribonucleotides
Organ Specificity
RNA, Messenger: IP, isolation & purification
*RNA, Messenger: ME, metabolism
Rats
Research Support, U.S. Gov't, P.H.S.

ANSWER 10 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AN 1999:516866 BIOSIS

DN PREV199900516866

TI Urinary excretion of fatty acid binding protein (**L-FABP**) reflects the stress on the proximal tubule and a marker of progression of **renal** damage.

AU Kamijo, A. [Reprint author]; Yamanouchi, M.; Sugaya, T.; Nomata, Y.; Hirano, N.; Hase, H.; Oba, S. [Reprint author]; Suzuki, N. [Reprint author]; Miyashita, K. [Reprint author]; Hirata, Y. [Reprint author]; Goto, A. [Reprint author]; Fujita, T. [Reprint author]; Omata, M. [Reprint author]; Kimura, K. [Reprint author]

CS Internal Medicine, University of Tokyo, Tokyo, Japan

SO Journal of the American Society of Nephrology, (Sept., 1999) Vol. 10, No. PROGRAM AND ABSTR. ISSUE, pp. 106A. print.
Meeting Info.: 32nd Annual Meeting of the American Society of Nephrology. Miami Beach, Florida, USA. November 1-8, 1999. American Society of Nephrology.
CODEN: JASNEU. ISSN: 1046-6673.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 3 Dec 1999
Last Updated on STN: 3 Dec 1999

CC Urinary system - Pathology 15506
Physiology - Stress 12008
Metabolism - Lipids 13006
Metabolism - Proteins, peptides and amino acids 13012
General biology - Symposia, transactions and proceedings 00520
Urinary system - Physiology and biochemistry 15504
Urinary system - Anatomy 15502
Biochemistry studies - Proteins, peptides and amino acids 10064
Biochemistry studies - Lipids 10066

IT Major Concepts
Nephrology (Human Medicine, Medical Sciences)

IT Chemicals & Biochemicals
L-fatty acid binding protein: proximal tubule stress reflection, **renal** damage progression marker, urinary excretion

IT Miscellaneous Descriptors
Meeting Abstract

ORGN Classifier
Hominidae 86215
Super Taxa
Primates; Mammalia; Vertebrata; Chordata; Animalia

ANSWER 9 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:359733 CAPLUS

DN 130:349390

ED Entered STN: 11 Jun 1999

TI Method for examining kidney diseases.

IN Yamanouchi, Masaya; Honda, Akiko; Uchida, Hiromi; Sugaya, Takeshi; Kimura, Kenjiro

PA Tanabe Seiyaku Co., Ltd., Japan

SO PCT Int. Appl., 31 pp.
CODEN: PIXXD2

DT Patent

LA Japanese

IC ICM G01N033-53

CC 9-10 (Biochemical Methods)
Section cross-reference(s): 14, 15

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9927363	A1	19990603	WO 1998-JP5319	19981126
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	TW 562926	B	20031121	TW 1998-87119150	19981119
	JP 11242026	A2	19990907	JP 1998-331828	19981124
	JP 3259768	B2	20020225		
	AU 9912603	A1	19990615	AU 1999-12603	19981126
	EP 1043587	A1	20001011	EP 1998-955936	19981126
	EP 1043587	B1	20030604		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	AT 242484	E	20030615	AT 1998-955936	19981126
PRAI	JP 1997-323684	A	19971126		
	WO 1998-JP5319	W	19981126		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 9927363	ICM	G01N033-53
WO 9927363	ECLA	G01N033/68V
EP 1043587	ECLA	G01N033/68V

AB A diagnostic method is described for examining kidney diseases by immunol. detecting a fatty acid-binding protein derived from ki

ANSWER 18 OF 20 EMBASE
on STN

AN 89265049 EMBASE
DN 1989265049
TI Mechanism of hepatic fatty acid uptake.
AU Stremmel W.
CS Abteilung fur Gastroenterologie des Zentrums fur Innere Medizin der Universitatskliniken Dusseldorf, 4000 Dusseldorf, Germany
SO Journal of Hepatology, (1989) 9/3 (374-382).
ISSN: 0168-8278 CODEN: JOHEEC
CY Netherlands
DT Journal
FS 029 Clinical Biochemistry
048 Gastroenterology
LA English
SL English
AB In recent years a new concept of the mechanism of hepatic fatty acid uptake has been described. It was shown that this major class of energy yielding substraters enters hepatocytes by a carrier-mediated uptake system. After the dissociation of the fatty acid-albumin complex at the sinusoidal **liver** cell **plasma** membrane, fatty acid binds with high affinity to a specific, newly identified, 40 kDa membrane **fatty acid binding protein** (MFABP). This protein functions as transmembrane transporter for long chain fatty acids. Hepatocellular uptake of fatty acids was shown to be sodium-dependent and electrogenic, compatible with a Na+-fatty acid cotransport system.
CT Medical Descriptors:
*cell membrane
*electrochemical gradient
***liver function**
*membrane transport
review
human
priority journal
Drug Descriptors:
*fatty acid

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review
human
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Drug Descriptors:
*fatty acid

ANSWER 15 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:188195 CAPLUS
DN 118:188195
ED Entered STN: 14 May 1993
TI **Liver plasma** membrane **fatty acid binding protein**
AU Potter, Barry J.; Berk, Paul D.
CS Dep. Med., Mount Sinai Sch. Med., New York, NY, 10029, USA
SO Hepatic Transp. Bile Secretion (1993), 253-67. Editor(s): Tavoloni, Nicola; Berk, Paul D. Publisher: Raven, New York, N. Y.
CODEN: 58QLAU
DT Conference; General Review
LA English
CC 13-0 (Mammalian Biochemistry)
AB A **review**, with 56 refs., on: cell surface events and the albumin receptor hypothesis; isolation of the **plasma** membrane **fatty acid-binding protein**; characterization of the **fatty acid-binding protein**; and if the **plasma** membrane **fatty acid binding protein** related to mitochondrial glutamic-oxalacetic transaminase.
ST **review liver fatty acid binding protein**
IT **Liver**, composition
(**fatty acid-binding proteins** of membrane of)
IT Cell membrane
(**fatty acid-binding proteins** of, of **liver**)
IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(FABP (**fatty acid-binding protein**), of **liver** cell membrane)

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ANSWER 12 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:88191 CAPLUS
DN 126:167969
ED Entered STN: 06 Feb 1997
TI **Fatty acid-binding proteins**. Their structure, function and gene expression
AU Fujii, Hiroshi
CS Sch. Med., Niigata Univ., Niigata, Japan
SO Domyaku Koka (1996), 24(7/8), 353-361
CODEN: DOMKDM; ISSN: 0386-2682
PB Nippon Domyaku Koka Gakkai
DT Journal; General Review
LA Japanese
CC 6-0 (General Biochemistry)
AB A **review** with 45 refs., on the mol. structures, genes, and biol. functions of **fatty acid-binding protein** (FABP). Lipid-binding, -transfer or -exchange proteins are present in intra- and extracellular fluids of all organisms. They play a role in the transport or targeting of lipids in the cell or in the **plasma**, but may also interact directly or indirectly by modulation of various cellular processes. The structure of these families of lipid-binding proteins, albumin, lipocalin and **fatty acid-binding protein** (FABP) families, has been established. FABP have similar mol. masses (14-15 kDa) and amino acid compns., exhibit some sequences similarity (38-70%), and form a family with other hydrophobic ligand-binding proteins such as cellular retinol-binding protein (CRBP), cellular retinoic acid-binding protein (CRABP) and intestinal bile acid-binding protein (I-BABP/I-15P/ILBP). At least, 7 types of FABP, **liver** (L), intestine (I), heart (H), brain (B), myelin (mP2), adipocyte (aP2) or skin type (E/C) FABP, have been isolated from various sources. The large similarity of H-HABP, aP2, mP2, and E/C-FABP (60-70%) is reflected in the similar amino acids on essential positions for fatty acid binding. Interestingly, these FABPs and CRBP I and II contain a protein tyrosine kinase recognition sequence before Tyr 19. The physiol. relevance of tyrosine phosphorylation of FABP remains unclear. Furthermore, recently, a significant degree of primary sequence similarity was noted between a domain of an ion channel, the N-methyl-D-aspartate receptor and the members of the FABP family, while the significance of FABP-like domain for ion channel regulation remains unknown. X-ray diffraction anal. of FABP family proteins revealed that the show a structure of 2 short α-helixes located near N terminus and followed by 10 anti-parallel β-strands. The β-strands are organized into 2 nearly orthogonal β-sheets giving the protein the overall appearance of a "clam shell". To date, the genes for 9 members of the FABP family have been identified. The overall organization of the genes is identical, 4 exons and 3 introns. The exon/intron boundaries are similar in all genes but the length of the intron sequences varies markedly. Although FABP has been thought to be involved in the intracellular transport and metabolism of long-chain fatty acids or other hydrophobic ligands, their physiol. roles in cells are not precisely understood. Intracellular fatty acids are important mols. for energy delivery and for synthesis of membrane lipid mediators such as eicosanoids. Apart from their functioning as metabolic substrates and constituents of complex lipids, long-chain fatty acids are being recognized as elements of several cell-to-cell signal transduction pathways. Therefore, it would be interesting to examine mechanisms of the action of FABP involved in these cellular signal transduction.
ST **review** FABP protein structure gene function
IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)

ANSWER 12 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:88191 CAPLUS
DN 126:167969
ED Entered STN: 06 Feb 1997
TI **Fatty acid-binding proteins**. Their structure, function and gene expression
AU Fujii, Hiroshi
CS Sch. Med., Niigata Univ., Niigata, Japan
SO Domyaku Koka (1996), 24(7/8), 353-361
CODEN: DOMKDM; ISSN: 0386-2682
PB Nippon Domyaku Koka Gakkai
DT Journal; General Review
LA Japanese
CC 6-0 (General Biochemistry)
AB A **review** with 45 refs., on the mol. structures, genes, and biol. functions of **fatty acid-binding protein** (FABP). Lipid-binding, -transfer or -exchange proteins are present in intra- and extracellular fluids of all organisms. They play a role in the transport or targeting of lipids in the cell or in the **plasma**, but may also interact directly or indirectly by modulation of various cellular processes. The structure of these families of lipid-binding proteins, albumin, lipocalin and **fatty acid-binding protein** (FABP) families, has been established. FABP have similar mol. masses (14-15 kDa) and amino acid compns., exhibit some sequences similarity (38-70%), and form a family with other hydrophobic ligand-binding proteins such as cellular retinol-binding protein (CRBP), cellular retinoic acid-binding protein (CRABP) and intestinal bile acid-binding protein (I-BABP/I-15P/ILBP). At least, 7 types of FABP, **liver** (L), intestine (I), heart (H), brain (B), myelin (mP2), adipocyte (aP2) or skin type (E/C) FABP, have been isolated from various sources. The large similarity of H-HABP, aP2, mP2, and E/C-FABP (60-70%) is reflected in the similar amino acids on essential positions for fatty acid binding. Interestingly, these FABPs and CRBP I and II contain a protein tyrosine kinase recognition sequence before Tyr 19. The physiol. relevance of tyrosine phosphorylation of FABP remains unclear. Furthermore, recently, a significant degree of primary sequence similarity was noted between a domain of an ion channel, the N-methyl-D-aspartate receptor and the members of the FABP family, while the significance of FABP-like domain for ion channel regulation remains unknown. X-ray diffraction anal. of FABP family proteins revealed that the show a structure of 2 short α-helixes located near N terminus and followed by 10 anti-parallel β-strands. The β-strands are organized into 2 nearly orthogonal β-sheets giving the protein the overall appearance of a "clam shell". To date, the genes for 9 members of the FABP family have been identified. The overall organization of the genes is identical, 4 exons and 3 introns. The exon/intron boundaries are similar in all genes but the length of the intron sequences varies markedly. Although FABP has been thought to be involved in the intracellular transport and metabolism of long-chain fatty acids or other hydrophobic ligands, their physiol. roles in cells are not precisely understood. Intracellular fatty acids are important mols. for energy delivery and for synthesis of membrane lipid mediators such as eicosanoids. Apart from their functioning as metabolic substrates and constituents of complex lipids, long-chain fatty acids are being recognized as elements of several cell-to-cell signal transduction pathways. Therefore, it would be interesting to examine mechanisms of the action of FABP involved in these cellular signal transduction.
ST **review** FABP protein structure gene function
IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)

(FABP (**fatty acid-binding protein**
); mol. structure, function, and gene expression of **fatty acid-binding proteins**)

IT Gene, animal
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(mol. structure, function, and gene expression of **fatty acid-binding proteins**)

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); mol. structure, function, and gene expression of **fatty acid-binding proteins**)

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(mol. structure, function, and gene expression of **fatty acid-binding proteins**)